

(FILE 'HOME' ENTERED AT 09:53:57 ON 08 FEB 2005)

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 09:54:01 ON 08 FEB  
2005

L1	58 S KLUYVEROMYCES (2N) AESTUARI
L2	8 S L1 AND (CARBONYL (2N) REDUCTASE)
L3	6 DUP REM L2 (2 DUPLICATES REMOVED)

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1539	100.0	292	3	US-09-468-738A-2	Sequence 2, Appli
2	1539	100.0	292	4	US-09-940-019-2	Sequence 2, Appli
3	1539	100.0	292	4	US-09-940-037A-2	Sequence 2, Appli
4	1539	100.0	296	3	US-09-468-738A-23	Sequence 23, Appl
5	1539	100.0	296	4	US-09-940-019-23	Sequence 23, Appl
6	1539	100.0	296	4	US-09-940-037A-23	Sequence 23, Appl
7	827	53.7	290	4	US-09-248-796A-16592	Sequence 16592, A
8	621	40.4	308	4	US-09-248-796A-16593	Sequence 16593, A
9	558.5	36.3	283	3	US-09-367-012-1	Sequence 1, Appli
10	558.5	36.3	283	4	US-09-777-157A-1	Sequence 1, Appli
11	363.5	23.6	316	4	US-09-489-039A-12990	Sequence 12990, A
12	337	21.9	257	3	US-09-134-001C-3562	Sequence 3562, Ap
13	294.5	19.1	111	4	US-09-248-796A-16591	Sequence 16591, A
14	289.5	18.8	251	4	US-09-922-501-16	Sequence 16, Appl
15	289.5	18.8	306	4	US-09-710-279-382	Sequence 382, App
16	288	18.7	254	4	US-09-978-758-2	Sequence 2, Appli
17	287.5	18.7	274	3	US-09-134-001C-4431	Sequence 4431, Ap
18	283.5	18.4	253	4	US-09-543-681A-6693	Sequence 6693, Ap

6, 416, 986

6, 485, 948

RESULT 2

US-09-940-019-2

; Sequence 2, Application US/09940019

; Patent No. 6416986

; GENERAL INFORMATION:

; APPLICANT: Kimoto, No. 6416986ihiro

; APPLICANT: Yamamoto, Hiroaki

; APPLICANT: Mitsushashi, Kazuya

; TITLE OF INVENTION: NOVEL CARBONYL REDUCTASE, METHOD FOR PRODUCING SAID ENZYME, DNA

; TITLE OF INVENTION: ENCODING SAID ENZYME, AND METHOD FOR PRODUCING ALCOHOL USING SAID

; TITLE OF INVENTION: ENZYME

; FILE REFERENCE: 06501-050001

; CURRENT APPLICATION NUMBER: US/09/940,019

; CURRENT FILING DATE: 2001-08-27

; PRIOR APPLICATION NUMBER: 09/468,738

; PRIOR FILING DATE: 1999-06-17

; PRIOR APPLICATION NUMBER: JP 1998-363130

; PRIOR FILING DATE: 1998-12-21

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn Ver. 2.0, reformatted using WordPerfect 5.1

; SEQ ID NO 2

; LENGTH: 292

; TYPE: PRT

; ORGANISM: Kluyveromyces aestuarii

US-09-940-019-2

Query Match 100.0%; Score 1539; DB 4; Length 292;

Best Local Similarity 100.0%; Pred. No. 1.1e-153;

Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTFQHFLRGGLEDKTVPQEPPKEQYPDGVNYLSLFSQKGKLTVITGGAGAIGGALCEGFA 60

|||||

Db 1 MTFQHFLRGGLEDKTVPQEPPKEQYPDGVNYLSLFSQKGKLTVITGGAGAIGGALCEGFA 60

RESULT 3

US-09-940-037A-2

```
; Sequence 2, Application US/09940037A
; Patent No. 6485948
; GENERAL INFORMATION:
; APPLICANT: Kimoto, No. 6485948ihiro
; APPLICANT: Yamamoto, Hiroaki
; APPLICANT: Mitsuhashi, Kazuya
; TITLE OF INVENTION: NOVEL CARBONYL REDUCTASE, METHOD FOR PRODUCING SAID
ENZYME, DNA
; TITLE OF INVENTION: ENCODING SAID ENZYME, AND METHOD FOR PRODUCING ALCOHOL
USING SAID
; TITLE OF INVENTION: ENZYME
; FILE REFERENCE: 06501-050001
; CURRENT APPLICATION NUMBER: US/09/940,037A
; CURRENT FILING DATE: 2000-08-27
; PRIOR APPLICATION NUMBER: 09/468,738
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: JP 1998-363130
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0, reformatted using WordPerfect 5.1
; SEQ ID NO 2
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Kluyveromyces aestuarii
US-09-940-037A-2
```

```
Query Match          100.0%; Score 1539; DB 4; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.1e-153;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 MTFQHFLRGGLEDKTVPQEPPKEQYPDGVNYLSLFSQKGKLTVITGGAGAIGGALCEGFA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MTFQHFLRGGLEDKTVPQEPPKEQYPDGVNYLSLFSQKGKLTVITGGAGAIGGALCEGFA 60
```

Database :       Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1539	100.0	292	9	US-09-940-019-2	Sequence 2, Appli
2	1539	100.0	292	9	US-09-940-037A-2	Sequence 2, Appli
3	1539	100.0	292	12	US-09-855-309-2	Sequence 2, Appli
4	1539	100.0	296	9	US-09-940-019-23	Sequence 23, Appl
5	1539	100.0	296	9	US-09-940-037A-23	Sequence 23, Appl
6	1539	100.0	296	12	US-09-855-309-23	Sequence 23, Appl
7	852	55.4	282	14	US-10-032-585-7746	Sequence 7746, Ap

Database : PIR\_79:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query		Length	DB	ID	Description
	Score	Match				
1	558.5	36.3	283	2	JC7338	carbonyl reductase
2	510.5	33.2	255	2	T39164	sorbitol utilizati
3	451.5	29.3	261	2	T41116	short chain dehydr
4	407	26.4	261	2	T38157	short-chain dehydr
5	396	25.7	257	2	A72395	oxidoreductase, sh
6	352.5	22.9	255	2	D70635	hypothetical prote
7	335.5	21.8	271	2	AC0157	probable short cha
8	331.5	21.5	262	2	AG2809	short chain dehydr
9	331.5	21.5	262	2	B97588	oxidoreductase, sh
10	313.5	20.4	282	1	JC4041	D-arabinitol 2-deh
11	303.5	19.7	281	2	F69400	2-deoxy-D-gluconat
12	301	19.6	298	2	AI3058	gluconate 5-dehydr

Database : UniProt\_02:\*.  
 1: uniprot\_sprot:\*.  
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	1534	99.7	292	2	Q75WS0	Q75ws0 kluyveromyc
2	1534	99.7	292	2	BAD01116	Bad01116 kluyverom
3	1289	83.8	292	2	Q6CM75	Q6cm75 kluyveromyc
4	864.5	56.2	286	2	Q6BXW6	Q6bxw6 debaryomyce
5	644	41.8	278	2	Q6CEE9	Q6cee9 yarrowia li
6	637	41.4	279	2	Q6BQ25	Q6bq25 debaryomyce
7	624	40.5	280	1	SOU2_CANAL	P87218 candida alb
8	622.5	40.4	281	1	SOU1_CANAL	P87219 candida alb
9	619	40.2	291	2	Q6BN16	Q6bn16 debaryomyce
10	607	39.4	280	2	Q6CM06	Q6cm06 kluyveromyc
11	605.5	39.3	285	2	Q6BQ28	Q6bq28 debaryomyce

RESULT 1

Q75WS0

ID Q75WS0 PRELIMINARY; PRT; 292 AA.  
AC Q75WS0;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Carbonyl reductase.  
GN Name=kacr1;  
OS Kluyveromyces aestuarii.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
OX NCBI\_TaxID=33165;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yamamoto H., Mitsuhashi K., Kimoto N., Matsuyama A., Esaki N.,  
RA Kobayashi Y.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.  
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
CC (SDR) family.  
DR EMBL; AB120765; BAD01116.1; -.  
DR InterPro; IPR002198; ADH\_short.  
DR InterPro; IPR002347; Adh\_short\_C2.  
DR Pfam; PF00106; adh\_short; 1.  
DR PRINTS; PR00081; GDHRDH.  
DR PRINTS; PR00080; SDRFAMILY.  
DR PROSITE; PS00061; ADH\_SHORT; UNKNOWN\_1.  
KW Oxidoreductase.  
SQ SEQUENCE 292 AA; 31685 MW; 0165CCCB430EF7DA CRC64;

Query Match 99.7%; Score 1534; DB 2; Length 292;  
Best Local Similarity 99.7%; Pred. No. 2.7e-113;  
Matches 291; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MTFQHFLRGGLEDKTVPEPPKEQYPDGVNYLSLFSQKGKLTVITGGAGAIGGALCEGFA	60
Db	1	MTFQHFLRGGLEDKTVPEPPKEQYPDGVNYLSLFSQKGKLTVITGGAGAIGGALCEGFA	60
Qy	61	SCGSDVVILDYKYSPELSSVLESRYGVRKSYQVDITSSQVKKLVVAKILEDFFPDRDINT	120
Db	61	SCGSDVVILDYKYSPELSSVLESRYGVRKSYQVDITSSQVKKLVVAKILEDFFPDRDINT	120
Qy	121	FVANAGIAWTNGSILNENATPDVWKRMDVNVQGTYHCAKYVAEVFKQQGHGNLILTASM	180
Db	121	FVANAGIAWTNGSILNENATPDVWKRMDVNVQGTYHCAKYVAEVFKQQGHGNLILTASM	180
Qy	181	SSYISNVPNYQTCYNASKAAVRHMAKGFVEFAHLTNPAGKIRCNSVSPGYTDTALSAFV	240
Db	181	SSYISNVPNYQTCYNASKAAVRHMAKGFVEFAHLTNPAGKIRCNSVSPGYTDTALSAFV	240
Qy	241	PVEQRAQWWGLTPMGREALPQELVGAYLYLASDAASFTNGCDIQVDGGYTCV	292
Db	241	PVEQRAQWWGLTPMGREALPQEXVGAYLYLASDAASFTNGCDIQVDGGYTCV	292